Patent Claims

1. Isolated polynucleotides containing at least one of the polynucleotide sequences selected from the group

   a) polynucleotide which is at least 70% identical to a polynucleotide which codes for a polypeptide containing at least one amino acid sequence of SEQ ID no. 3 or 5,

   b) polynucleotide which codes for a polypeptide which contains an amino acid sequence which is at least 70% identical to the amino acid sequence of SEQ ID no. 3 or 5,

   c) polynucleotide which is complementary to the polynucleotides of a), b) or c), and

   d) polynucleotide containing at least 15 successive bases of the polynucleotide sequences of a), b) or c).

2. The polynucleotide as claimed in claim 1, wherein the polynucleotide is a preferably recombinant DNA replicable in coryneform bacteria.

3. The polynucleotide as claimed in claim 1, wherein the polynucleotide is an RNA.

4. The replicable DNA as claimed in claim 2, containing

   (i) one of the nucleotide sequences shown in SEQ ID no. 1 or SEQ ID no. 6, or

   (ii) at least one sequence which matches the sequence (i) within the degeneration range of the genetic code, or

(iii) at least one sequence which hybridises with the complementary sequence to sequence (i) or (ii) and optionally

(iv) functionally neutral sense mutations in (i).

5. Amino acid sequence of the protein derived from the nucleotide sequences as claimed in claims 1 or 2 shown in SEQ ID no. 2 and SEQ ID no. 4.

6. Coryneform microorganisms, in particular of the genus Corynebacterium, transformed by the introduction of one or more of the replicable DNA as claimed in one of claims 2 or 5.

7. Process for the production of branched-chain L-amino acids by fermentation of coryneform bacteria,
w h e r e i n
bacteria are used in which the brnE and/or brnF gene or nucleotide sequences coding for these genes are amplified, in particular overexpressed.

8. The process as claimed in claim 7,
w h e r e i n
bacteria are used in which further genes of the biosynthetic pathway of the desired L-amino acid are additionally amplified.

9. The process as claimed in claim 7,
w h e r e i n
bacteria are used in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partially suppressed.

10. The process as claimed in claims 8 to 10,
w h e r e i n
a strain transformed with one or more plasmid vectors is used and the plasmid vector(s) bear(s) the nucleotide sequences which code for the brnE and/or

brnF gene.

11. The process as claimed in one or more of claims 8 to 10,
w h e r e i n
coryneform bacteria are used which produce L-isoleucine, L-valine or L-leucine.

12. A process for the production of branched-chain L-amino acids,
w h e r e i n
the following steps are performed:

a) fermentation of microorganisms as claimed in one or more of the preceding claims, in which microorganisms at least the brnE and/or brnF gene, optionally in combination with further genes, is amplified, in particular overexpressed,

b) accumulation of the desired L-amino acid in the medium or in the cells of the microorganisms and

c) isolation of the L-amino acid.

13. The process as claimed in one or more of the preceding claims,
w h e r e i n
microorganisms of the genus Corynebacterium are used.

14. A process for isolating the brnE or brnF gene,
w h e r e i n
mutants, preferably coryneform bacteria, which are defective in this/these gene(s) are obtained as indicator strains which do not grow or grow only slightly on a nutrient medium containing oligopeptide containing isoleucine and/or leucine and/or valine and

a) once a gene library has been constructed, the brnE or brnF gene is identified and isolated, or

in the case of transposon mutagenesis, selection is performed for the transposon preferably containing antibiotic resistance and the desired genes are consequently obtained.